

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/674,817

DATE: 05/08/2001  
TIME: 11:50:03

Input Set : A:\ES.txt  
Output Set: N:\CRF3\05082001\I674817.raw

**ENTERED**

3 <110> APPLICANT: Lorz, et al.  
 5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT AND  
 6 WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH  
 8 <130> FILE REFERENCE: 514413-3849  
 10 <140> CURRENT APPLICATION NUMBER: 09/674,817  
 C--> 11 <141> CURRENT FILING DATE: 2001-04-06  
 13 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03141  
 14 <151> PRIOR FILING DATE: 1999-05-07  
 16 <150> PRIOR APPLICATION NUMBER: 19820608.9  
 17 <151> PRIOR FILING DATE: 1998-05-08  
 19 <160> NUMBER OF SEQ ID NOS: 10  
 21 <170> SOFTWARE: PatentIn version 3.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 2997  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Triticum aestivum L. cv. Florida  
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 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (3)..(296)  
 31 <223> OTHER INFORMATION: exon 1  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: CDS  
 36 <222> LOCATION: (2145)..(2921)  
 37 <223> OTHER INFORMATION: exon 3  
 40 <220> FEATURE:  
 41 <221> NAME/KEY: Intron  
 42 <222> LOCATION: (297)..(396)  
 43 <223> OTHER INFORMATION: intron 1  
 46 <220> FEATURE:  
 47 <221> NAME/KEY: CDS  
 48 <222> LOCATION: (397)..(1617)  
 49 <223> OTHER INFORMATION: exon 2  
 52 <220> FEATURE:  
 53 <221> NAME/KEY: Intron  
 54 <222> LOCATION: (1618)..(2144)  
 55 <223> OTHER INFORMATION: intron 2  
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 59 gg tcg ggg ccg gcg ccg cgc ctg cga cgg tgg cga ccc aat gcg acg 47  
 60 Ser Gly Pro Ala Pro Arg Leu Arg Arg Trp Arg Pro Asn Ala Thr  
 61 1 5 10 15  
 63 gcg ggg aag ggg gtc ggc gag gtg tgc gcc gcg gtt gtc gag gcg gcg 95  
 64 Ala Gly Lys Gly Val Gly Glu Val Cys Ala Ala Val Val Glu Ala Ala  
 65 20 25 30  
 67 acg aag gta gag gac gag ggg gag gag gac gag ccg gtg gcg gag gac 143  
 68 Thr Lys Val Glu Asp Glu Gly Glu Asp Glu Pro Val Ala Glu Asp  
 69 35 40 45  
 71 agg tac gcg ctc ggc ggc tgc agg gtg ctc gcc gga atg ccc gcg 191

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72	Arg	Tyr	Ala	Leu	Gly	Gly	Ala	Cys	Arg	Val	Leu	Ala	Gly	Met	Pro	Ala	
73	50			55					60								
75	ccg	ctg	ggc	gcc	acc	gca	gtc	gcc	ggc	ggg	gtc	aat	ttc	gcc	gtc	tat	239
76	Pro	Leu	Gly	Ala	Thr	Ala	Leu	Ala	Gly	Gly	Val	Asn	Phe	Ala	Val	Tyr	
77	65			70					75								
79	tcc	ggc	gga	gcc	acc	gca	gca	gtc	gtc	gtc	ttc	acg	cca	gaa	gat		287
80	Ser	Gly	Gly	Ala	Thr	Ala	Ala	Ala	Leu	Cys	Leu	Phe	Thr	Pro	Glu	Asp	
81	80			85					90				95				
83	ctc	aag	gca	gtggggttgc	ctcccgagta	gagttcatca	gctttgcgtg										336
84	Leu	Lys	Ala														
87	cggccgcgc	cccttttttgc	ccctctgcaat	ttaagttttgc	tactggggca	aatgtgcag											396
89	gat	agg	gtg	acc	gag	gag	gtt	ccc	ctt	gac	ccc	ctg	atg	aat	cgg	acc	444
90	Asp	Arg	Val	Thr	Glu	Glu	Val	Pro	Leu	Asp	Pro	Leu	Met	Asn	Arg	Thr	
91	100			105					110								
93	ggg	aac	gtg	tgg	cat	gtc	ttc	atc	gaa	ggc	gag	ctg	cac	aac	atg	ctt	492
94	Gly	Asn	Val	Trp	His	Val	Phe	Ile	Glu	Gly	Glu	Leu	His	Asn	Met	Leu	
95	115			120					125				130				
97	tac	ggg	tac	agg	ttc	gac	ggc	acc	ttt	gct	cct	cac	tgc	ggg	cac	tac	540
98	Tyr	Gly	Tyr	Arg	Phe	Asp	Gly	Thr	Phe	Ala	Pro	His	Cys	Gly	His	Tyr	
99	135			140					145								
101	ctt	gat	gtt	tcc	aat	gtc	gtg	gtg	gat	cct	tat	gct	aag	gca	gtg	ata	588
102	Leu	Asp	Val	Ser	Asn	Val	Val	Val	Asp	Pro	Tyr	Ala	Lys	Ala	Val	Ile	
103	150			155					160								
105	agc	cga	ggg	gag	tat	ggt	gtt	cca	gca	gtc	cgt	ggt	aac	aat	tgc	tgg	636
106	Ser	Arg	Gly	Glu	Tyr	Gly	Val	Pro	Ala	Arg	Gly	Asn	Asn	Cys	Trp	Pro	
107	165			170					175								
109	cag	atg	gct	ggc	atg	atc	cct	ctt	cca	tat	agc	acg	ttt	gat	tgg	gaa	684
110	Gln	Met	Ala	Gly	Met	Ile	Pro	Leu	Pro	Tyr	Ser	Thr	Phe	Asp	Trp	Glu	
111	180			185					190								
113	ggc	gac	cta	cct	cta	aga	tat	cct	caa	aag	gac	ctg	gta	ata	tat	gag	732
114	Gly	Asp	Leu	Pro	Leu	'Arg	Tyr	Pro	Gln	Lys	Asp	Leu	Val	Ile	Tyr	Glu	
115	195			200					205				210				
117	atg	cac	ttg	cgt	gga	ttc	acg	aag	cat	gat	tca	agc	aat	gta	gaa	cat	780
118	Met	His	Leu	Arg	Gly	Phe	Thr	Lys	His	Asp	Ser	Ser	Asn	Val	Glu	His	
119	215			220					225								
121	ccg	ggc	act	ttc	att	gga	gct	gtg	tcg	aag	ctt	gac	tat	ttg	aag	gag	828
122	Pro	Gly	Thr	Ile	Gly	Ala	Val	Ser	Lys	Leu	Asp	Tyr	Leu	Lys	Glu		
123	230			235					240								
125	ctt	gga	gtt	aat	tgt	att	gaa	tta	atg	ccc	tgc	cat	gag	ttc	aac	gag	876
126	Leu	Gly	Val	Asn	Cys	Ile	Glu	Leu	Met	Pro	Cys	His	Glu	Phe	Asn	Glu	
127	245			250					255								
129	ctg	gag	tac	tca	acc	tct	tct	tcc	aag	atg	aac	ttt	tgg	gga	tat	tct	924
130	Leu	Glu	Tyr	Ser	Thr	Ser	Ser	Ser	Lys	Met	Asn	Phe	Trp	Gly	Tyr	Ser	
131	260			265					270								
133	acc	ata	aac	ttc	ttt	tca	cca	atg	aca	aga	tac	aca	tca	ggc	ggg	ata	972
134	Thr	Ile	Asn	Phe	Phe	Ser	Pro	Met	Thr	Arg	Tyr	Thr	Ser	Gly	Gly	Ile	
135	275			280					285				290				
137	aaa	aac	tgt	ggg	cgt	gat	gcc	ata	aat	gag	ttc	aaa	act	ttt	gta	aga	1020
138	Lys	Asn	Cys	Gly	Arg	Asp	Ala	Ile	Asn	Glu	Phe	Lys	Thr	Phe	Val	Arg	

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139	295	300	305		
141	gag gct cac aaa	cgg gga att gag	gtg atc ctg gat	gtt gtc ttc aac	1068
142	Glu Ala His Lys	Arg Gly Ile Glu Val	Ile Leu Asp Val	Val Phe Asn	
143	310	315	320		
145	cat aca gct gag	ggt aat gag aat	ggt cca ata tta	tca ttt aag ggg	1116
146	His Thr Ala Glu	Gly Asn Glu Asn	Gly Pro Ile	Leu Ser Phe Lys Gly	
147	325	330	335		
149	gtc gat aat act aca	tac tat atg ctt	gca ccc aag	gga gag ttt tat	1164
150	Val Asp Asn Thr	Thr Tyr Tyr Met	Leu Ala Pro	Lys Gly Glu Phe Tyr	
151	340	345	350		
153	aac tat tct ggc	tgt ggg aat acc	tcc aac tgt	aat cat cct gtg gtt	1212
154	Asn Tyr Ser Gly	Cys Gly Asn Thr	Phe Asn Cys	Asn His Pro Val Val	
155	355	360	365	370	
157	cgt caa ttc att	gta gat tgt tta	aga tac tgg	gtg acg gaa atg cat	1260
158	Arg Gln Phe Ile	Val Asp Cys Leu	Arg Tyr Trp Val	Thr Glu Met His	
159	375	380	385		
161	gtt gat ggt ttt	cgt ttt gat ctt	gca tcc ata	atg acc aga ggt tcc	1308
162	Val Asp Gly Phe	Arg Phe Asp Leu	Ala Ser Ile	Met Thr Arg Gly Ser	
163	390	395	400		
165	agt ctg tgg gat	cca gtt aac	gtg tat gga	gct cca ata gaa ggt gac	1356
166	Ser Leu Trp Asp	Pro Val Asn Val	Tyr Gly Ala Pro	Ile Glu Gly Asp	
167	405	410	415		
169	atg atc aca aca	ggg aca cct	ctt gtt act	cca cca ctt att gac atg	1404
170	Met Ile Thr Thr	Gly Thr Pro	Leu Val Thr	Pro Pro Leu Ile Asp Met	
171	420	425	430		
173	atc agc aat gac	cca att ctt	gga ggc gtc	aag ctc att gct gaa gca	1452
174	Ile Ser Asn Asp	Pro Ile Leu Gly	Gly Val Lys	Leu Ile Ala Glu Ala	
175	435	440	445	450	
177	tgg gat gca	gga ggc ctc	tat caa gta	ggt caa ttc cct cac tgg aat	1500
178	Trp Asp Ala	Gly Leu Tyr	Gln Val Gly	Gln Phe Pro His Trp Asn	
179	455	460	465		
181	gtt tgg tct	gag tgg aat	ggg aag tac	cgg gac att gtg cgt caa ttc	1548
182	Val Trp Ser	Glu Trp Asn Gly	Lys Tyr Arg Asp	Ile Val Arg Gln Phe	
183	470	475	480		
185	att aaa ggc act	gat gga ttt	gct ggt ggt	ttt gcc gaa tgt ctt tgt	1596
186	Ile Lys Gly	Thr Asp Gly Phe	Ala Gly	Gly Phe Ala Glu Cys Leu Cys	
187	485	490	495		
189	gga agt cca	cac cta tac	cag gtaagttgt	gcaatacttg taaatgagg	1647
190	Gly Ser Pro His	Leu Tyr Gln			
191	500	505			
193	gaggtaatgt	cacctggatt	tttttatatat	accacatgat gatacacatc	1707
195	acaatcatag	tgtatgcata	tgcatttggc	taagaagtagt tagtgtatac	1767
197	tatatagggt	ttaacaccca	acttgc当地	gaaggaacat agggcttct agttatctta	1827
199	tttatttgc	cggtaataa	tccactgaaa	aattccagcc atgtcatttt ttaggggggg	1887
201	agaagaaact	atattgattt	gccccctaa	aagaagccat ctc当地ataggtaa	1947
203	tgc当地tgc	taaagaaagg	aaaacgactt	catactttct atcgggtgcta acttagctcg	2007
205	atgtatattt	gtaagatgaa	tgc当地attt	aatttgc当地ataatttgat ctgttattca	2067
207	caaatttcta	tttggatttct	ctagaaatca	aaccagtaac ttgttattgg cactgcaact	2127
209	tcttatttgc	taatcag	gca gga agg	aaa cct tgg cac agt atc aac	2177

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210	Ala	Gly	Gly	Arg	Lys	Pro	Trp	His	Ser	Ile	Asn						
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213	ttt	tgt	gca	cat	gat	gga	ttt	aca	ctg	gct	gat	ttg	gta	aca	tat	2225	
214	Phe	Val	Cys	Ala	His	Asp	Gly	Phe	Thr	Leu	Ala	Asp	Leu	Val	Thr	Tyr	
215					520				525			530					
217	aat	aag	aac	aat	tta	cca	aat	ggg	gag	aac	aac	aga	aat	gga	gaa	2273	
218	Asn	Lys	Lys	Tyr	Asn	Leu	Pro	Asn	Gly	Glu	Asn	Asn	Arg	Asp	Gly	Glu	
219					535				540			545					
221	aat	cac	aat	ctt	agc	tgg	aat	tgt	ggg	gag	gaa	gga	ttc	gca	aga	2321	
222	Asn	His	Asn	Leu	Ser	Trp	Asn	Cys	Gly	Glu	Glu	Gly	Glu	Phe	Ala	Arg	
223					550				555			560					
225	ttg	tct	gtc	aaa	aga	ttg	agg	aag	agg	cag	atg	cgc	aat	ttc	ttt	gtt	2369
226	Leu	Ser	Val	Lys	Arg	Leu	Arg	Lys	Arg	Gln	Met	Arg	Asn	Phe	Phe	Val	
227	565				570				575			580					
229	tgt	ctc	atg	gtt	tct	caa	gga	gtt	cca	atg	ttc	tac	atg	ggt	gat	gaa	2417
230	Cys	Leu	Met	Val	Ser	Gln	Gly	Val	Pro	Met	Phe	Tyr	Met	Gly	Asp	Glu	
231					585				590			595					
233	tat	ggc	cac	aca	aaa	ggg	ggc	aac	aac	aat	aca	tac	tgc	cat	gat	tct	2465
234	Tyr	Gly	His	Thr	Lys	Gly	Gly	Asn	Asn	Asn	Thr	Tyr	Cys	His	Asp	Ser	
235					600				605			610					
237	tat	gtc	aat	tat	ttt	cgc	tgg	gat	aaa	aaa	gaa	caa	tac	tct	gag	ttg	2513
238	Tyr	Val	Asn	Tyr	Phe	Arg	Trp	Asp	Lys	Lys	Glu	Glu	Gly	Tyr	Ser	Glu	Leu
239					615				620			625					
241	cac	cga	ttc	tgc	tgc	ctc	atg	acc	aaa	ttc	cgc	aag	gag	tgc	gag	ggt	2561
242	His	Arg	Phe	Cys	Cys	Leu	Met	Thr	Lys	Phe	Arg	Lys	Glu	Cys	Glu	Gly	
243					630				635			640					
245	ctt	ggc	ctt	gag	gac	ttt	cca	acg	gcc	aaa	cg	ctg	cag	tgg	cat	ggt	2609
246	Leu	Gly	Leu	Glu	Asp	Phe	Pro	Thr	Ala	Lys	Arg	Leu	Gln	Trp	His	Gly	
247	645				650				655			660					
249	cat	cag	cct	ggg	aag	cct	gat	tgg	tct	gag	aat	agc	cga	ttc	gtt	gcc	2657
250	His	Gln	Pro	Gly	Lys	Pro	Asp	Trp	Ser	Glu	Asn	Ser	Arg	Phe	Val	Ala	
251					665				670			675					
253	ttt	tcc	atg	aaa	gat	gaa	aga	cag	ggc	gag	atc	tat	gtg	gcc	ttc	aac	2705
254	Phe	Ser	Met	Lys	Asp	Glu	Arg	Gln	Gly	Glu	Ile	Tyr	Val	Ala	Phe	Asn	
255					680				685			690					
257	acc	agc	cac	tta	ccg	gcc	gtt	gtt	gag	ctc	cca	gag	cgc	gca	ggg	cgc	2753
258	Thr	Ser	His	Leu	Pro	Ala	Val	Val	Glu	Leu	Pro	Glu	Arg	Ala	Gly	Arg	
259					695				700			705					
261	cg	tgg	gaa	ccg	gt	gt	gac	aca	ggc	aag	cca	gca	cca	tac	gac	ttc	2801
262	Arg	Trp	Glu	Pro	Val	Val	Asp	Thr	Gly	Lys	Pro	Ala	Pro	Tyr	Asp	Phe	
263					710				715			720					
265	ctc	acc	gac	gac	tta	cct	gat	cgc	gct	ctc	acc	ata	cac	cag	ttc	tcg	2849
266	Leu	Thr	Asp	Asp	Leu	Pro	Asp	Arg	Ala	Leu	Thr	Ile	His	Gln	Phe	Ser	
267	725				730				735			740					
269	cat	ttc	ctc	tac	tcc	aac	ctc	tac	ccc	atg	ctc	agc	tac	tca	tcg	gtc	2897
270	His	Phe	Leu	Tyr	Ser	Asn	Leu	Tyr	Pro	Met	Leu	Ser	Tyr	Ser	Ser	Val	
271					745				750			755					
273	atc	cta	gta	ttg	ccg	cct	gat	gtt	tgagagacca	atatatacag	ataataat	ataataat	ataataat	ataataat	ataataat	ataataat	2951
274	Ile	Leu	Val	Leu	Arg	Pro	Asp	Val									

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281	<211>	LENGTH: 764		
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283	<213>	ORGANISM: Triticum aestivum L. cv. Florida		
285	<400>	SEQUENCE: 2		
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292	20	25	30	
295	Lys Val Glu Asp Glu Gly Glu Asp Glu Pro Val Ala Glu Asp Arg			
296	35	40	45	
299	Tyr Ala Leu Gly Gly Ala Cys Arg Val Leu Ala Gly Met Pro Ala Pro			
300	50	55	60	
303	Leu Gly Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr Ser			
304	65	70	75	80
307	Gly Gly Ala Thr Ala Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp Leu			
308	85	90	95	
311	Lys Ala Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn			
312	100	105	110	
315	Arg Thr Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu His Asn			
316	115	120	125	
319	Met Leu Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly			
320	130	135	140	
323	His Tyr Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala			
324	145	150	155	160
327	Val Ile Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys			
328	165	170	175	
331	Trp Pro Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp			
332	180	185	190	
335	Trp Glu Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile			
336	195	200	205	
339	Tyr Glu Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val			
340	210	215	220	
343	Glu His Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu			
344	225	230	235	240
347	Lys Glu Leu Gly Val Asn Cys Ile Glu Leu Met Pro Cys His Glu Phe			
348	245	250	255	
351	Asn Glu Leu Glu Tyr Ser Thr Ser Ser Lys Met Asn Phe Trp Gly			
352	260	265	270	
355	Tyr Ser Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr Ser Gly			
356	275	280	285	
359	Gly Ile Lys Asn Cys Gly Arg Asp Ala Ile Asn Glu Phe Lys Thr Phe			
360	290	295	300	
363	Val Arg Glu Ala His Lys Arg Gly Ile Glu Val Ile Leu Asp Val Val			
364	305	310	315	320
367	Phe Asn His Thr Ala Glu Gly Asn Glu Asn Gly Pro Ile Leu Ser Phe			
368	325	330	335	

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date